

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/500,872
Source: PCT
Date Processed by STIC: 2-17-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/24/05



PCT

RAW SEQUENCE LISTING

DATE: 02/17/2005

PATENT APPLICATION: US/10/500,872

TIME: 12:20:46

Input Set : A:\NOB-8 Seq List (28902.0008).txt

Output Set: N:\CRF4\02172005\J500872.raw

4 <110> APPLICANT: OP DEN CAMP, Hubertus Johannes Marie
 5 HARHANGI, Harry Ramanoedj
 6 VAN DER DRIFT, Christiaan
 7 PRONK, Jacobus Thomas
 9 <120> TITLE OF INVENTION: Fermentation of pentose sugars
 11 <130> FILE REFERENCE: 28902.0008
 13 <140> CURRENT APPLICATION NUMBER: 10/500,872
 14 <141> CURRENT FILING DATE: 2004-07-07
 16 <150> PRIOR APPLICATION NUMBER: PCT/NL03/00049
 17 <151> PRIOR FILING DATE: 2003-01-23
 19 <150> PRIOR APPLICATION NUMBER: BO 44829
 20 <151> PRIOR FILING DATE: 2001-12-31
 22 <160> NUMBER OF SEQ ID NOS: 4
 24 <170> SOFTWARE: PatentIn Ver. 2.1

1- ss Not 100%
 Corrected (pg. 2-4)

ERRORED SEQUENCES

26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 437
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Piromyces sp.
 31 <400> SEQUENCE: 1
 33 Met Ala Lys Glu Tyr Phe Pro Gln Ile Gln Lys Ile Lys Phe Glu Gly
 34 1 5 10 15
 36 Lys Asp Ser Lys Asn Pro Leu Ala Phe His Tyr Tyr Asp Ala Glu Lys
 37 20 25 30
 39 Glu Val Met Gly Lys Lys Met Lys Asp Trp Leu Arg Phe Ala Met Ala
 40 35 40 45
 42 Trp Trp His Thr Leu Cys Ala Glu Gly Ala Asp Gln Phe Gly Gly Gly
 43 50 55 60
 45 Thr Lys Ser Phe Pro Trp Asn Glu Gly Thr Asp Ala Ile Glu Ile Ala
 46 65 70 75 80
 48 Lys Gln Lys Val Asp Ala Gly Phe Glu Ile Met Gln Lys Leu Gly Ile
 49 85 90 95
 51 Pro Tyr Tyr Cys Phe His Asp Val Asp Leu Val Ser Glu Gly Asn Ser
 52 100 105 110
 54 Ile Glu Glu Tyr Glu Ser Asn Leu Lys Ala Val Val Ala Tyr Leu Lys
 55 115 120 125
 57 Glu Lys Gln Lys Glu Thr Gly Ile Lys Leu Leu Trp Ser Thr Ala Asn
 58 130 135 140
 60 Val Phe Gly His Lys Arg Tyr Met Asn Gly Ala Ser Thr Asn Pro Asp
 61 145 150 155 160

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63 Phe Asp Val Val Ala Arg Ala Ile Val Gln Ile Lys Asn Ala Ile Asp
64      165      170      175
E--> 66 Ala Gly Ile Glu Leu Gly Ala Glu Asn Tyr Val Phe Trp Gly Gly Arg
67      180      185      190
69 Glu Gly Tyr Met Ser Leu Leu Asn Thr Asp Gln Lys Arg Glu Lys Glu
70      195      200      205
72 His Met Ala Thr Met Leu Thr Met Ala Arg Asp Tyr Ala Arg Ser Lys
73      210      215      220
75 Gly Phe Lys Gly Thr Phe Leu Ile Glu Pro Lys Pro Met Glu Pro Thr
76 225      230      235      240
78 Lys His Gln Tyr Asp Val Asp Thr Glu Thr Ala Ile Gly Phe Leu Lys
79      245      250      255
81 Ala His Asn Leu Asp Lys Asp Phe Lys Val Asn Ile Glu Val Asn His
82      260      265      270
84 Ala Thr Leu Ala Gly His Thr Phe Glu His Glu Leu Ala Cys Ala Val
85      275      280      285
87 Asp Ala Gly Met Leu Gly Ser Ile Asp Ala Asn Arg Gly Asp Tyr Gln
88      290      295      300
90 Asn Gly Trp Asp Thr Asp Gln Phe Pro Ile Asp Gln Tyr Glu Leu Val
91 305      310      315      320
93 Gln Ala Trp Met Glu Ile Ile Arg Gly Gly Gly Phe Val Thr Gly Gly
94      325      330      335
96 Thr Asn Phe Asp Ala Lys Thr Arg Arg Asn Ser Thr Asp Leu Glu Asp
97      340      345      350
99 Ile Ile Ile Ala His Val Ser Gly Met Asp Ala Met Ala Arg Ala Leu
100      355      360      365
102 Glu Asn Ala Ala Lys Leu Leu Gln Glu Ser Pro Tyr Thr Lys Met Lys
103      370      375      380
105 Lys Glu Arg Tyr Ala Ser Phe Asp Ser Gly Ile Gly Lys Asp Phe Glu
106 385      390      395      400
108 Asp Gly Lys Leu Thr Leu Glu Gln Val Tyr Glu Tyr Gly Lys Lys Asn
109      405      410      415
111 Gly Glu Pro Lys Gln Thr Ser Gly Lys Gln Glu Leu Tyr Glu Ala Ile
112      420      425      430
114 Val Ala Met Tyr Gln
115      435
182 <210> SEQ ID NO: 3
183 <211> LENGTH: 494
184 <212> TYPE: PRT
185 <213> ORGANISM: Piromyces sp.
187 <400> SEQUENCE: 3
189 Met Lys Thr Val Ala Gly Ile Asp Leu Gly Thr Gln Ser Met Lys Val
190 1      5      10      15
192 Val Ile Tyr Asp Tyr Glu Lys Lys Glu Ile Ile Glu Ser Ala Ser Cys
193      20      25      30
195 Pro Met Glu Leu Ile Ser Glu Ser Asp Gly Thr Arg Glu Gln Thr Thr
196      35      40      45
198 Glu Trp Phe Asp Lys Gly Leu Glu Val Cys Phe Gly Lys Leu Ser Ala
199      50      55      60

```

*Invalid
Amino
Acid*

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201 Asp Asn Lys Lys Thr Ile Glu Ala Ile Gly Ile Ser Gly Gln Leu His
 202 65 70 75 80
 204 Gly Phe Val Pro Leu Asp Ala Asn Gly Lys Ala Leu Tyr Asn Ile Lys
 205 85 90 95
 207 Leu Trp Cys Asp Thr Ala Thr Val Glu Glu Cys Lys Ile Ile Thr Asp
 208 100 105 110
 210 Ala Ala Gly Gly Asp Lys Ala Val Ile Asp Ala Leu Gly Asn Leu Met
 211 115 120 125
 213 Leu Thr Gly Phe Thr Ala Pro Lys Ile Leu Trp Leu Lys Arg Asn Lys
 214 130 135 140
 216 Pro Glu Ala Phe Ala Asn Leu Lys Tyr Ile Met Leu Pro His Asp Tyr
 217 145 *What is this?* 150 155 160
 219 Leu Asn Trp Lys Leu Thr Gly Asp Tyr Val Met Glu Tyr Gly Asp Ala
 220 165 170 175
 E--> 222 Ser Gly Thr *A h* Leu Phe Asp Ser Lys Asn Arg Cys Trp Ser Lys Lys
 E--> 223 180 185 190
 225 Ile Cys Asp Ile Ile Asp Pro Lys Leu Leu Asp Leu Leu Pro Lys Leu
 226 195 200 205
 228 Ile Glu Pro Ser Ala Pro Ala Gly Lys Val Asn Asp Glu Ala Ala Lys
 229 210 215 220
 231 Ala Tyr Gly Ile Pro Ala Gly Ile Pro Val Ser Ala Gly Gly Gly Asp
 232 225 230 235 240
 234 Asn Met Met Gly Ala Val Gly Thr Gly Thr Val Ala Asp Gly Phe Leu
 235 245 250 255
 237 Thr Met Ser Met Gly Thr Ser Gly Thr Leu Tyr Gly Tyr Ser Asp Lys
 238 260 265 270
 240 Pro Ile Ser Asp Pro Ala Asn Gly Leu Ser Gly Phe Cys Ser Ser Thr
 241 275 280 285
 243 Gly Gly Trp Leu Pro Leu Leu Cys Thr Met Asn Cys Thr Val Ala Thr
 244 290 295 300
 246 Glu Phe Val Arg Asn Leu Phe Gln Met Asp Ile Lys Glu Leu Asn Val
 247 305 310 315 320
 249 Glu Ala Ala Lys Ser Pro Cys Gly Ser Glu Gly Val Leu Val Ile Pro
 250 325 330 335 *ASN*
 E--> 252 Phe Phe Asn Gly Glu Arg Thr Pro Asn Leu Pro *A s n* Gly Arg Ala Ser
 E--> 253 340 345 350
 255 Ile Thr Gly Leu Thr Ser Ala Asn Thr Ser Arg Ala Asn Ile Ala Arg
 256 355 360 365
 258 Ala Ser Phe Glu Ser Ala Val Phe Ala Met Arg Gly Leu Asp Ala
 259 370 375 380
 261 Phe Arg Lys Leu Gly Phe Gln Pro Lys Glu Ile Arg Leu Ile Gly Gly
 262 385 390 395 400
 264 Gly Ser Lys Ser Asp Leu Trp Arg Gln Ile Ala Ala Asp Ile Met Asn
 265 405 410 415
 267 Leu Pro Ile Arg Val Pro Leu Leu Glu Glu Ala Ala Ala Leu Gly Gly
 268 420 425 430
 270 Ala Val Gln Ala Leu Trp Cys Leu Lys Asn Gln Ser Gly Lys Cys Asp
 271 435 440 445
 273 Ile Val Glu Leu Cys Lys Glu His Ile Lys Ile Asp Glu Ser Lys Asn

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OK 274 450 455 460 Lys
276 Ala Asn Pro Ile Ala Glu Asn Val Ala Val Tyr Asp LYS Ala Tyr Asp
OK 277 465 470 475 480
279 Glu Tyr Cys Lys Val Val Asn Thr Leu Ser Pro Leu Tyr Ala
OK 280 485 490

↑
tyr errors shown exist the
heseq errors. Please check the
sequences for similar errors.

VERIFICATION SUMMARY

DATE: 02/17/2005

PATENT APPLICATION: US/10/500,872

TIME: 12:20:47

Input Set : A:\NOB-8 Seq List (28902.0008).txt

Output Set: N:\CRF4\02172005\J500872.raw

L:66 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1 ✓

L:222 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓

L:222 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:2 ✓

L:223 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 ✓

M:332 Repeated in SeqNo=3

L:252 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓

L:252 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:3 ✓

L:280 M:252 E: No. of Seq. differs, <211> LENGTH:Input:494 Found:497 SEQ:3 ✓